

9598-066

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ACGTTGACAC	AGGAATGAAG	AGTGTATTGG	CTGAATCTTC	AAGCAGAGGC	GATATTGACC	60
ATGTGCTTTT	TAAATTGGCC	TGCGTGACCC	GCCCACCTGG	TGTAAAAGAA	GAACCGGCCA	120
AAGGGAGGGC	CTGAAGGACC	TCCACAGGAG	TGTGAGCAGC	ACTGCTTCAG	CAACAAAGCC	180
TCAGGTCCAC	ATCTTGGGAA	GAAT	ATG GCC ACT TCC TGG GGG GCT GTC TTC			231
		Met	Ala Thr Ser Trp Gly Ala Val Phe			
		1		5		
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG		279				
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln						
10	15	20				
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT		327				
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn						
30	35	40				
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT		375				
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr						
45	50	55				
GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG		423				
Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln						
60	65	70				
CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT		471				
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu						
75	80	85				
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG		519				
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu						
90	95	100				
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG		567				
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg						
110	115	120				
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG		615				
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu						
125	130	135				
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT		663				
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn						
140	145	150				
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC		711				
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser						
155	160	165				
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG		759				
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln						
170	175	180				
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT		807				
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly						
190	195	200				
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA		855				
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu						
205	210	215				
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT		903				
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr						
220	225	230				

Fig. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	
235 240 245	
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	
250 255 260	265
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	
270 275 280	
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG	1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Glu Met	
285 290 295	
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	
300 305 310	
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	
315 320 325	
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	
330 335 340	345
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	
350 355 360	
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG	1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met	
365 370 375	
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Lys Asp Gly Leu Gly Phe Ala	
380 385 390	
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC	1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp	
395 400 405	
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT	1479
Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His	
410 415 420 425	
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA	1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	
430 435 440	
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT	1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	
445 450 455	
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT	1629
Gly Lys Ala Trp Pro Glu Thr Arg	
460 465	

Fig. 1 (cont'd.)

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TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCTTTTGGGA	1749
TTCTTTGTAC	AGAGTCCTGC	AAAGGAAAAA	AGAGAAAAGG	TTTGGAATC	CATGCTAGAT	1809
TGCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAAT	CTCGTTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTCG	TTATAAGCTG	ATTACTGAA	ATCCCATAAC	1929
CCATCAATGC	TGTTAATTTT	TTCTTCCTA	CCCTTATTAC	ATCCCTACC	CTAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTG	CTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

Fig. 1 (cont'd.)

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peaNTase 1 ---MELFHKDTTFLTEMPAITSQYQGNHLSRTTFKQZBIASVAVFDAGSTGSR
potapyrase 1 GLNQNSHTFPHQHMFLVLPLSLLSKNVAQPPRRHLSHESE..HYAVTFDAGSTGSR
mNTase 1 MATSMGATFMQIACMGCTVFYRQQTWFEQYFLSSNCFINVSAGTFYQTFDAGSTGSR
yGDPase 1 KFPKXISLTFENDEFGQLQDSEKTEQNYPELADAVKSQTSQTCSEHRYVIMFDAGSTGSR

peaNTase 57 IHVYHSENMCDLHIGKGYEYHKTFGLSSYAHMEQAAKSLPBLEQAEDEVVPDLOP
potapyrase 59 VHVTFPDEKLCCLDIGNNIYFNMTEFGLSSYAHMEQAAKSLPBLEQAEDEVVPDLOP
mNTase 61 IHVYTFVOKTAGQLFFDEGSEFFDMMFGLSATVQOPKQCAETVQELLEVAKDSIPRSHWE
yGDPase 61 VHVYKEDVCTG..EPTLDEKFMLEFGLSSIDTQSVGAANSQWPLLKVMNYVPIKARS

peaNTase 117 STPVLEGATAGLRRLNGDASEKILQSVRDMLSNRSTF.NVQPDNVSIMQCTQEGSYLVWT
potapyrase 119 ETPDEGGATAGLRMLKGDMEKILQAVRNLYKNQSTF.HSKDQWVHLQGNQCGSYMWAN
mNTase 121 EPTVYKATAGLRRLPEKQAQALLLEVEKTFNN.SPF.LVFPDGSVSIMDCSYECILARVT
yGDPase 119 CPTVAKATAGLRRLGDASKSKILSAVRDELEKDYTFEYVSGDGVSTMGDEGVYAWMTN

peaNTase 176 VNYALGHLGKNTN..TVGVIDLGGGSVOMAYAVSKNKAAPKADGMDPYLKKVYKQ
potapyrase 178 INYLLGHLGKNDKKS..TTATIDLGGGSVOMAYAVSKNKAAPKADGMDPYLKKVYKQ
mNTase 179 VNYLLGHLGKNGQE..DVCTLDGGASVOMAYAVSKNKAAPKADGMDPYLKKVYKQ
yGDPase 179 TNYLLGHLGKNGANGKPLFAAVFDLGGGSVOMAYAVSKNKAAPKADGMDPYLKKVYKQ

peaNTase 234 IPYGLYVHSYLFGRHASRAEILNL.....EPRSPRQCILACFNGIY
potapyrase 235 KPYGLYVHSYLYCOLAGRAEILFA.....EPRSPRQCILACFNGIY
mNTase 232 STEKLYTHSYLGFGLKAGLATGA.....EPRSPRQCILACFNGIY
yGDPase 234 ENYTLIQFSEHLGFGLEGRNKNVNSVLVENALKDGKILKGDNTKREQLSEPCFPFKVMTN

peaNTase 276 TVSGEPEKATAYTSQ.....NFMKCNITIRKALKNYFQPYQNTFCGMWNGGGG...
potapyrase 277 SVGGVRYKVKPKKQS.....SMKRCRDLTRKALKNYFQPYQNTFCGMWNGGGG...
mNTase 270 KCEPRNLEENITQGV.....KQYQGWQEGSGWGFPCYAKVLRVVGSKDHQPEEV...
yGDPase 294 EKYTLSEKPEYITIDFIQPDHFGAGQCFDIDBIUNKDQGGQSPPGSGVHQPSLVETFK

peaNTase 328 GKNHASSSEMYLPEOTCHVDSTPNFMNPVDIEKAKSACALNEZDARKSIFPDEKK
potapyrase 329 GKNHASSSEMYLPEOTCHVDSTPNFMNPVDIEKAKSACALNEZDARKSIFPDEKK
mNTase 322 GSA.FYAFSVYVDRADTHEDYE.KGGVDEVEDERKAREVCH.HGSPSSGSP...
yGDPase 354 ESNDLYIFSYFDRFLGMLAFPLNEENDLARIVCKGEETATVAVESCHAGS...DDLL

peaNTase 388 NYASVYCHDLIYQVYLLVDGFGDPLQKITGCKELEYQNAIVEAANPLGNATPAISALPF
potapyrase 389 NA.FLCHDLIYRHTLLVDGFGDPLQKITGCKELEYQNAIVEAANPLGNATPAISALPF
mNTase 374 ...FLCHDLIYRHTLLVDGFGDPLQKITGCKELEYQNAIVEAANPLGNATPAISALPF
yGDPase 411 ESDEHFCDDLSFYVSLHTQEDFPLQREHRTCKNHNK...ICNCLGASHPPLGNADNW

peaNTase 448 FERTMYFV-----
potapyrase 448 FERTMYFV-----
mNTase 430 PSSTSEACISEPVFSQEGVDSETFSDLSGKANPETR*
yGDPase 467 RCKKQSA-----

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FIG. 2

**ACR II**

**ACR III**

**ACR IV**

F16.3

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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA	60
AAGACCGGCT GCCGCCTGCT CCCCAGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC	120
GCGCGGTGCA TGGAAATGGG TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA	180
AAAACGAGCT ACATTTTTC A CAGCCGCAG CACGGTCCTT GGCAACAAG G ATG AGA	237
Met Arg	
1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4

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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCCTC CTGTCCTGGA CGTGA CTCTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC TGGCATCAGC CTCTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC	1697 1757 1817

Fig. 4 (cont'd.)

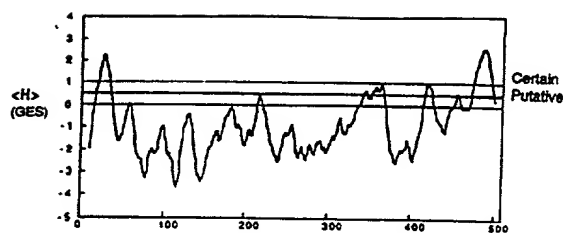
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AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAAACC	ACAGGCACCT	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGCTG	CAGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	TGCGATGGG	AGCTTTGTCT	CCCAGCTTGT	GCGTTTCCTC	1997
CCCAGGGCAG	AGCTCCCTTT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCTTGGCTG	2057
CTCTGGGGAA	CGCGAGGGAC	AGGCTATAACA	CCCCGGGGAC	AGTAGATGTG	CGCGGCACCA	2117
CTGGGAACTC	TGGACTTTAG	TGCTTTTGGT	TTCTCTTGGG	TATGAATTCT	TGAGTTTACC	2177
CAGAGGCCGT	CTCTCCTCAC	ACATTGTGTG	GTTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCAATAGC	GGCAGGTGCC	ACACCTTACG	GGAGTGTCTC	AGCATGGGCG	GATGCGCGGC	2297
ATGAGCTGCT	GTAACCTATT	TGTGGCTGTG	TGCTTTGAGT	GACGTCCTCT	TGCTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GGAGCTGTTC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACC	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCA	CCTCGGGCTG	ACCCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCCTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTCCGG	GCTGAGCCCC	TTGAGTGCTT	TCAGTGAATG	2657
TACAGTGCCC	GGCACGAGCT	GAACTCTCAT	TGTTCCACTC	CCAATAAAGG	GTTGACAGGG	2717
GCTTCTCCTT	CAAAAAAATA	AAAAAATAAA	AAAAAATAAA	AAAAA		2762

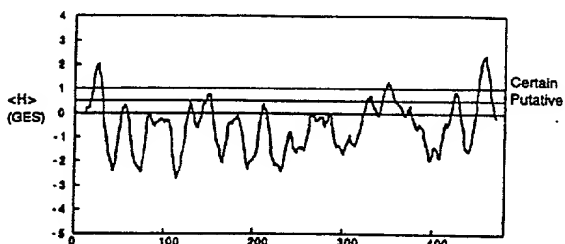
FIG. 4 (cont'd)



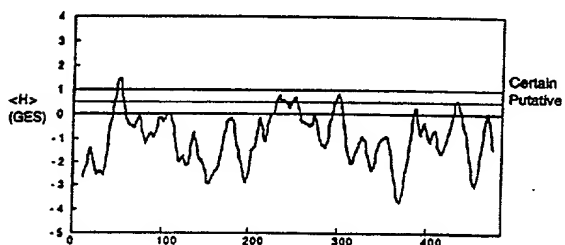
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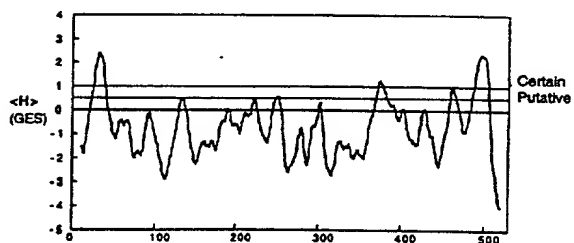
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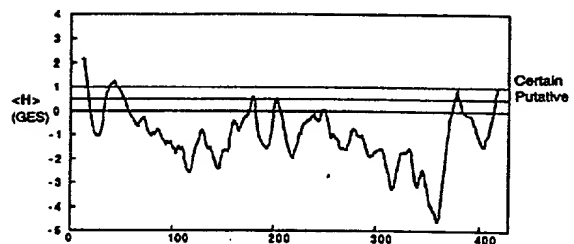
CD39L2



CD39L3



CD39L4



Amino acid position

FIG. 5

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ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG	60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT	112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys	
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC	160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC	208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT	256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA	304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165 170	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	

Fig. 6

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	
235 240 245 250	
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	
255 260 265	
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	
365 370 375	
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser	
380 385 390	
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC	1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu	
395 400 405 410	
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn	
415 420 425	
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr	
430 435 440	
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala	
445 450 455	
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA	1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	
460 465 470	
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	
475 480 485 490	

FIG. 6 (cont'd.)

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CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC	1703
Asp His Ala Val Asp Ser Asp	
525	
TGCTTAGAGT CAGCCTGGGT GGCACCAAGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA	1763
TACAACTAAC TAAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC	1823
AGCACCTCTT GAGGCATCCC TTGGCTATTC TGTGCATATT GTTCTTCAGA GACCTCACTA	1883
CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA	1943
TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATTG	2003
ACCTCAGGGC TCAGTTTCCA TTTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA	2063
AGCATTTTCG CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT	2123
TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAATAT AGTATCTGGG	2183
GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA	2243
TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG	2303
GAATTCACAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGTC ATCATCCTCA	2363
TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT	2423
GCATTCCAGA TTTTACTGCC TTTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTCCATT	2483
GTTATCATGG TGTATATATT TTTGTCACCA TTCCACAAG TATACTTGAT GTTGTCATAG	2543
AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT	2603
GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC	2663
TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAACTA AAAATCAGCA	2723
TTATTTTATA TTGCTGTTT TTAGCTGAAT ATGGAATAAA GAATATTAT TTTATTTTGA	2783
AAAAAAAAAA AAAA	2797

FIG. 6 (cont'd.)

GCGCGCGCGT	TTTCCTTGTT	CCTGGTCAAC	AAAGAAATGT	GGAGTGTCTT	GGCTGAATCC	60
TCATACAGAC	AAGATCATT	TGGTGCTGTT	AGGTAGGACT	TGTATCCAGA	TGTAAGGTTG	120
AAAAAGTGAT	ATAATAAGG	AACCAAGGAG	AAAATTCAGA	AGGAAAGAAA	AAATTGCCTC	180
TGCAGGTGTG	CGAGCAGGAT	TGCTTCTGCA	ACAAAAGCCT	CCACCCAGCC	ACATCTTGGG	240
AAAAGA ATG	GCC ACT TCT	TGG GGC ACA	GTC TTT TTC	ATG CTG GTG	GTA	288
Met	Ala Thr Ser Trp	Gly Thr Val Phe	Phe Met Leu Val	Val		
1		5		10		
TCC TGT GTT	TGC AGC GCT	GTC TCC CAC	AGG AAC CAG	CAG ACT TGG	TTT	336
Ser Cys Val	Cys Ser Ala	Val Ser His	Arg Asn Gln	Gln Thr Trp	Phe	
15		20		25	30	
GAG GGT ATC	TTC CTG TCT	TCC ATG TGC	CCC ATC AAT	GTC AGC GCC	AGC	384
Glu Gly Ile	Phe Leu Ser	Ser Met Cys	Pro Ile Asn	Val Ser Ala	Ser	
	35		40		45	
ACC TTG TAT	GGA ATT ATG	TTT GAT GCA	GGG AGC ACT	GGA ACT CGA	ATT	432
Thr Leu Tyr	Gly Ile Met	Phe Asp Ala	Gly Ser Thr	Gly Thr Arg	Ile	
	50		55		60	
CAT GTT TAC	ACC TTT GTG	CAG AAA ATG	CCA GGA CAG	CTT CCA ATT	CTA	480
His Val Tyr	Thr Phe Val	Gln Lys Met	Pro Gly Gln	Leu Pro Ile	Leu	
	65		70		75	
GAA GGG GAA	GTT TTT GAT	TCT GTG AAG	CCA GGA CTT	TCT GCT TTT	GTA	528
Glu Gly Glu	Val Phe Asp	Ser Val Lys	Pro Gly Leu	Ser Ala Phe	Val	
	80		85		90	
GAT CAA CCT	AAG CAG GGT	GCT GAG ACC	GTT CAA GGG	CTC TTA GAG	GTG	576
Asp Gln Pro	Lys Gln Gly	Ala Glu Thr	Val Gln Gly	Leu Leu Glu	Val	
	95		100		105	
GCC AAA GAC	TCA ATC CCC	CGA AGT CAC	TGG AAA AAG	ACC CCA GTG	GTC	624
Ala Lys Asp	Ser Ile Pro	Arg Ser His	Trp Lys Lys	Thr Pro Val	Val	
	115		120		125	
CTA AAG GCA	ACA GCA GGA	CTA CGC TTA	CTG CCA GAA	CAC AAA GCC	AAG	672
Leu Lys Ala	Thr Ala Gly	Leu Arg Leu	Leu Pro Glu	His Lys Ala	Lys	
	130		135		140	
GCT CTG CTC	TTT GAG GTA	AAG GAG ATC	TTC AGG AAG	TCA CCT TTC	CTG	720
Ala Leu Leu	Phe Glu Val	Lys Glu Ile	Phe Arg Lys	Ser Pro Phe	Leu	
	145		150		155	
GTA CCA AAG	GGC AGT GTT	AGC ATC ATG	GAT GGA TCC	GAC GAA GGC	ATA	768
Val Pro Lys	Gly Ser Val	Ser Ile Met	Asp Gly Ser	Asp Glu Gly	Ile	
	160		165		170	
TTA GCT TGG	GTT ACT GTG	AAT TTT CTG	ACA GGT CAG	CTG CAT GGC	CAC	816
Leu Ala Trp	Val Thr Val	Asn Phe Leu	Thr Gly Gln	Leu His Gly	His	
	175		180		185	
AGA CAG GAG	ACT GTG GGG	ACC TTG GAC	CTA GGG GGA	GCC TCC ACC	CAA	864
Arg Gln Glu	Thr Val Gly	Thr Leu Asp	Leu Gly Gly	Ala Ser Thr	Gln	
	195		200		205	
ATC ACG TTC	CTG CCC CAG	TTT GAG AAA	ACT CTG GAA	CAA ACT CCT	AGG	912
Ile Thr Phe	Leu Pro Gln	Phe Glu Lys	Thr Leu Glu	Gln Thr Pro	Arg	
	210		215		220	
GGC TAC CTC	ACT TCC TTT	GAG ATG TTT	AAC AGC ACT	TAT AAG CTC	TAT	960
Gly Tyr Leu	Thr Ser Phe	Glu Met Phe	Asn Ser Thr	Tyr Lys Leu	Tyr	
	225		230		235	

Fig. 7

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ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	
255 260 265 270	
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	
275 280 285	
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	
290 295 300	
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	
305 310 315	
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	
320 325 330	
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	
335 340 345 350	
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG	1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu	
355 360 365	
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC	1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr	
370 375 380	
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC	1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385 390 395	
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400 405 410	
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC	1539
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415 420 425	
GTA CTT CTTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG	1599
TTTCTGAACT AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT	1659
TACACATCTA ATGTGAACTG CTGCCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA	1719
TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTTAACCTTG GAGTGAGAGC	1779
CCAGGGACAG GTCCTTGAA ACCAAAGAAA AATCGCATTT CAACCCTTG AGTGCCTCAT	1839
TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGGTAACTG ACTTATTGCA ATCCCAAGAC	1899
CCATCAATAT CAGTATTTTT TTCTCCCTA TACAGTGCCC TGCCCACCCT TATCTGCACC	1959
CACCTCCCCT GAAAAAGAGA GAAAAAATA AAAAAAATA	1998

Fig. 7 (cont'd.)

CD39L2 1 MKEGIRYETSRKTSYIFQQPQHGPMQTRMKIKSHGSLRVAKVATPLGCVGVYHYVYR  
 CD39L4 1 -----  
 CD39L1 1 -----  
 CD39L3 1 -----  
 CD39 1 -----

CD39L2 61 KNEKATAGQFFSITRANPTKMGQAS.SPLGTAAGHNVFYGLDAGSGCTRVGVVQ  
 CD39L4 7 TVFFKLVVSCCSANSHRNOQTAFQGFSSKCPNVSAITLYGLDAGSGCTRVGVVQ  
 CD39L1 1 ---MKQVETDPPFLDRAKGLASLLGVNRPVPPPKYGIULDAGSSHTSSEYK  
 CD39L3 16 KATIRHPTIAGVGLKIVVLSITHQIKKAVLPPPKYGIULDAGSSHTSSEYK  
 CD39 7 SHKMPCEHNLNIGFMSIIAVIALALGOLDONKALPENVKYGIULDAGSSHTSSEYK

CD39L2 120 FT.KPFRKFTSEKFKVN.PG.SAYAD.V.K.AQ.FELQ.VAKODIPTDMKATPL  
 CD39L4 67 FVQKMPQOLNICEVDSVF.PG.SAYAD.PK.AQ.FELQ.VAKODIPTDMKATPL  
 CD39L1 58 NPAEKENDTGIVQHSQDVPCCISVADHPG.LQGLVGLDQDDEPREMKTPE  
 CD39L3 75 NPAEKENDTGIVQHSQDVPCCISVADHPG.LQGLVGLDQDDEPREMKTPE  
 CD39 67 NPAEKENDTGIVQHSQDVPCCISVADHPG.LQGLVGLDQDDEPREMKTPE

CD39L2 178 VLEKATAG.RIL...KGRAC...LKYNE.PK.SPFLVQDDCVSINACTECVQKITIN  
 CD39L4 126 VLEKATAG.RIL...KGRAC...LKYNE.PK.SPFLVQDDCVSINACTECVQKITIN  
 CD39L1 116 VLGATAGHRLLELTPKATSVIPLVTHLTQYFF..DFRGAHPSGOECVGLGATPHY  
 CD39L3 135 VLGATAGHRLLELTPKATSVIPLVTHLTQYFF..DFRGAHPSGOECVGLGATPHY  
 CD39 127 VLGATAGHRLLELTPKATSVIPLVTHLTQYFF..DFRGAHPSGOECVGLGATPHY

CD39L2 235 PTESL.....STPGSEVGLDLCG.STGIZFLPRVETLKAASPPSYLTALR  
 CD39L4 183 PTESL.....STPGSEVGLDLCG.STGIZFLPRVETLKAASPPSYLTALR  
 CD39L1 176 KLENK.YGVWVGRF...KOTGA.DLGGASTGITTETTSFEDRASE...L.DLGL  
 CD39L3 193 KLENK.YGVWVGRF...KOTGA.DLGGASTGITTETTSFEDRASE...L.DLGL  
 CD39 185 KLENK.YGVWVGRF...KOTGA.DLGGASTGITTETTSFEDRASE...L.DLGL

CD39L2 283 NETYKLVHLSLGLLNGARLA.LGATGQDPLDGLVUSPGLSPSPKSETHKAVTR  
 CD39L4 231 NETYKLVHLSLGLLNGARLA.LGATGQDPLDGLVUSPGLSPSPKSETHKAVTR  
 CD39L1 229 VQCHPETHSHSLCHQDGLQDPLDGLVUSPGLSPSPKSETHKAVTR  
 CD39L3 246 VQCHPETHSHSLCHQDGLQDPLDGLVUSPGLSPSPKSETHKAVTR  
 CD39 242 VQCHPETHSHSLCHQDGLQDPLDGLVUSPGLSPSPKSETHKAVTR

CD39L2 341 VEGKAAASSELCAANVSEVQDR.HRTSEVAVNDVYAFSVYDLAGVSEPAKKGGS  
 CD39L4 290 VEGKAAASSELCAANVSEVQDR.HRTSEVAVNDVYAFSVYDLAGVSEPAKKGGS  
 CD39L1 283 PCTADRPVWNSGERSLSGSSNPELSELVHSGPSHSS.PKSCPHGVQDVPVGR  
 CD39L3 307 LTVQDDES.MKQDVITFCSESLSEKVSINDKADQCTEPFGVQDVPVGR  
 CD39 300 PCT..KQFE.TLPQQFELSGCHTQOCNSLLEPNTMC.PKSCPHGVQDVPVGR

CD39L2 403 LTVQDDEPAKIVCALETPQSSPFGCHD.VYV.LDLOX.TP.PKSKVILKTRKDRVE  
 CD39L4 350 LTVQDDEPAKIVCALETPQSSPFGCHD.VYV.LDLOX.TP.PKSKVILKTRKDRVE  
 CD39L1 342 EV.....AFSAFYTLPLRTSMGLPVALLQKRAAVVYVQKQKQ  
 CD39L3 367 EV.....AFSAFYTLPLRTSMGLPVALLQKRAAVVYVQKQKQ  
 CD39 357 EV.....AFSAFYTLPLRTSMGLPVALLQKRAAVVYVQKQKQ

CD39L2 462 KSWALGALPHI.DQNEQKSP[S\*-----  
 CD39L4 410 KSWALGALPHI.DQNEQKSP[S\*-----  
 CD39L1 384 .....DLISRGYGDERRTGGIFPKRA.....KGVGLGYHLLHNTIPAMPFG  
 CD39L3 418 KSTYCFKTHYHFGNGYVETETATPCDHPHETVNSHLLKGVGLGYHLLHNTIPAMPFG  
 CD39 409 LSTYCFKTHYHFGNGYVETETATPCDHPHETVNSHLLKGVGLGYHLLHNTIPAMPFG

CD39L2 485 -----  
 CD39L4 429 -----  
 CD39L1 432 KKKOTFESHVVVQDDEPAKIVCALETPQSSPFGCHD.VYV.LDLOX.TP.PKSKVILKTRKDRVE  
 CD39L3 478 KKKOTFESHVVVQDDEPAKIVCALETPQSSPFGCHD.VYV.LDLOX.TP.PKSKVILKTRKDRVE  
 CD39 466 KKKOTFESHVVVQDDEPAKIVCALETPQSSPFGCHD.VYV.LDLOX.TP.PKSKVILKTRKDRVE

FIG. 8

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peaGDP 1 -----  
 potapyrase 1 -----  
 CD39L2 1 MKKGIRYETSRKTSYIFQQPQHGPMQTRMKEKHHGSLRVAIVYPLGLCVGVYIYHQN  
 CD39L4 1 -----  
 dNTPase 1 -----  
 yGDPase 1 -----

## ACR I

peaGDP 2 ELLMLITPFEPSPISSOYLENMLLTSEKIFEEISSYAPFDAGSTGSRHVY  
 potapyrase 6 SHPTFILLFLVLESLSLSKVNAQIPRRHLLSESEYAFADAGSTGSRVHV  
 CD39L2 61 KWRATATQAYESTRPGARAGQAEKSPKAAQHEVYVIMFDAGSTGRVHV  
 CD39L4 7 TEFLLVVCUCSAVRRHQSTFEQHLSEPCFNVASITLYIMFDAGSTGRHVY  
 dNTPase 37 KTSFUCIISVILDLVVFQVSEMAFELRLSKFGYBKVOYALADAGSTGSRVLA  
 yGDPase 5 DHSIIPNDEFGYQDSKLEONFPLADAKSQSQCSEERVYIMFDAGSTGSRVLY

## ACR II

peaGDP 61 EFNOMLDLLEISKGEYKTPGLSSYAPFOAANSLPLLQEDVVDOLQPKTPV  
 potapyrase 63 EFNKLDLLEISKGEYKTPGLSSYAPFOAANSLPLLQEDVVDOLQPKTPV  
 CD39L2 119 QFTHEPRETPTTHETKAVKPGCLSYADDTUEKAGRELLDVANQDFFQPKATP  
 CD39L4 66 TTVORPGQLSILECEVFDVKPCLSYVQDQKAEICGLVAKESPESEKATP  
 dNTPase 96 KFNRSFIDMKLVYKELKPKPCLSSADPAKESKLLDEAATPESEKATP  
 yGDPase 65 KETCTSEITLLEKEDMPEGLSSDTSVCAANSLPLLQVAMTVPKARSCPEV

## ACR II

## ACR III

peaGDP 121 KCCATAGLRLLNGDAEKILOVRDLSSSTFNVFPAVSI DGTCEGSHLVTVHYA  
 potapyrase 123 KCCATAGLRLLNGDAEKILOVRDLSSSTFNVFPAVSI DGTCEGSHLVTVHYA  
 CD39L2 178 VLKATAGLRLLNGDAEKILOVRDLSSSTFNVFPAVSI DGTCEGSHLVTVHYA  
 CD39L4 126 VLKATAGLRLLNGDAEKILOVRDLSSSTFNVFPAVSI DGTCEGSHLVTVHYA  
 dNTPase 156 VLKATAGLRLLNGDAEKILOVRDLSSSTFNVFPAVSI DGTCEGSHLVTVHYA  
 yGDPase 123 ALKATAGLRLLNGDAEKILOVRDLSSSTFNVFPAVSI DGTCEGSHLVTVHYA

## ACR IV

peaGDP 180 LGNLCGRNYSFVGVDLGGGSGVAAVSKKTAKNAPVADGDPVYKVVUKGIFZH  
 potapyrase 182 LGNLCGRNYSFVGVDLGGGSGVAAVSKKTAKNAPVADGDPVYKVVUKGIFZH  
 CD39L2 236 TCELEKTPGOSVGVDLGGGSGVAAVSKKTAKNAPVADGDPVYKVVUKGIFZH  
 CD39L4 184 TCELEKTPGOSVGVDLGGGSGVAAVSKKTAKNAPVADGDPVYKVVUKGIFZH  
 dNTPase 214 LGNLCGRNYSFVGVDLGGGSGVAAVSKKTAKNAPVADGDPVYKVVUKGIFZH  
 yGDPase 183 LGNLCGRNYSFVGVDLGGGSGVAAVSKKTAKNAPVADGDPVYKVVUKGIFZH

peaGDP 238 LYVHSYLGECRAARRAPLNLTFEGE.....KPCILAGPNC.....Y  
 potapyrase 239 LYVHSYLGECRAARRAPLNLTFEGE.....KPCILAGPNC.....Y  
 CD39L2 289 LYVHSYLGECRAARRAPLNLTFEGE.....KPCILAGPNC.....Y  
 CD39L4 237 LYVHSYLGECRAARRAPLNLTFEGE.....KPCILAGPNC.....Y  
 dNTPase 264 LYVHSYLGECRAARRAPLNLTFEGE.....KPCILAGPNC.....Y  
 yGDPase 238 LYVHSYLGECRAARRAPLNLTFEGE.....KPCILAGPNC.....Y

peaGDP 276 TVSGEIRNAITNGHEMELCMTIRALKLRIFCPYONCTFGGWNCG...SGMGQRN  
 potapyrase 277 TVSGEIRNAITNGHEMELCMTIRALKLRIFCPYONCTFGGWNCG...SGMGQRN  
 CD39L2 335 TVSGEIRNAITNGHEMELCMTIRALKLRIFCPYONCTFGGWNCG...SGMGQRN  
 CD39L4 282 TVSGEIRNAITNGHEMELCMTIRALKLRIFCPYONCTFGGWNCG...SGMGQRN  
 dNTPase 308 TVSGEIRNAITNGHEMELCMTIRALKLRIFCPYONCTFGGWNCG...SGMGQRN  
 yGDPase 298 TVSGEIRNAITNGHEMELCMTIRALKLRIFCPYONCTFGGWNCG...SGMGQRN

peaGDP 332 LAGSSFLDPLDTGHRVDASTPNTLTVLEIKAKEACALHEDARS...PLDKHYV  
 potapyrase 333 LAGSSFLDPLDTGHRVDASTPNTLTVLEIKAKEACALHEDARS...PLDKHYV  
 CD39L2 379 LAGSSFLDPLDTGHRVDASTPNTLTVLEIKAKEACALHEDARS...PLDKHYV  
 CD39L4 326 LAGSSFLDPLDTGHRVDASTPNTLTVLEIKAKEACALHEDARS...PLDKHYV  
 dNTPase 360 LAGSSFLDPLDTGHRVDASTPNTLTVLEIKAKEACALHEDARS...PLDKHYV  
 yGDPase 358 LAGSSFLDPLDTGHRVDASTPNTLTVLEIKAKEACALHEDARS...PLDKHYV

peaGDP 392 FLCHDLITQIVLLVDGFGCLHFLKRTSSKMTIQAAVEAANPLCAVLAASLPKERR  
 potapyrase 392 FLCHDLITQIVLLVDGFGCLHFLKRTSSKMTIQAAVEAANPLCAVLAASLPKERR  
 CD39L2 428 FLCHDLITQIVLLVDGFGCLHFLKRTSSKMTIQAAVEAANPLCAVLAASLPKERR  
 CD39L4 375 FLCHDLITQIVLLVDGFGCLHFLKRTSSKMTIQAAVEAANPLCAVLAASLPKERR  
 dNTPase 406 FLCHDLITQIVLLVDGFGCLHFLKRTSSKMTIQAAVEAANPLCAVLAASLPKERR  
 yGDPase 415 FLCHDLITQIVLLVDGFGCLHFLKRTSSKMTIQAAVEAANPLCAVLAASLPKERR

peaGDP 452 MYFV  
 potapyrase 452 MYFV  
 CD39L2 483 MYFV  
 CD39L4 429 MYFV  
 dNTPase 462 MYFV  
 yGDPase 471 MYFV

Fig. 9